

CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule encoding a stress-related polypeptide, wherein the polypeptide binds in a yeast two hybrid assay to a fragment of a protein selected from the group consisting of OsGF14-c (SEQ ID NO: 113), OsDAD1 (SEQ ID NO: 128), Os006819-2510 (SEQ ID NO: 20), OsCRTC (SEQ ID NO: 134), OsSGT1 (SEQ ID NO: 144), OsERP (SEQ ID NO: 146), OsCHIB1 (SEQ ID NO: 152), OsCS (SEQ ID NO: 156), OsPP2A-2 (SEQ ID NO: 164), and OsCAA90866 (SEQ ID NO: 170).
2. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule is derived from rice (*Oryza sativa*).
3. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of odd numbered SEQ ID NOs: 1-111.
4. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of odd numbered SEQ ID NOs: 1-15 and the protein comprises an amino acid sequence of SEQ ID NO: 114.
5. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of SEQ ID NOs: 7 and 17 and the protein comprises an amino acid sequence of SEQ ID NO: 128.
6. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of odd numbered SEQ ID NOs: 21-25 and the protein comprises an amino acid sequence of SEQ ID NO: 20.
7. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 27 and the protein comprises an amino acid sequence of SEQ ID NO: 134.

8. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 29 and the protein comprises an amino acid sequence of SEQ ID NO: 138.

5 9. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of odd numbered SEQ ID NOs: 31-43 and the protein comprises an amino acid sequence of SEQ ID NO: 144.

10 10. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of odd numbered SEQ ID NOs: 45-67 and the protein comprises an amino acid sequence of SEQ ID NO: 146.

11. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 69 and the protein comprises an amino acid sequence of SEQ ID NO: 36.

15 12. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of odd numbered SEQ ID NOs: 71-77 and the protein comprises an amino acid sequence of SEQ ID NO: 152.

20 13. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of odd numbered SEQ ID NOs: 79-95 and the protein comprises an amino acid sequence of SEQ ID NO: 156.

25 14. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of odd numbered SEQ ID NOs: 97-105 and the protein comprises an amino acid sequence of SEQ ID NO: 164.

30 15. The isolated nucleic acid molecule of claim 3, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of odd numbered SEQ ID NOs: 97 and 107-111 and the protein comprises an amino acid sequence of SEQ ID NO: 170.

16. An isolated nucleic acid molecule encoding a stress-related polypeptide, wherein the nucleic acid molecule is selected from the group consisting of:

- 5 (a) a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence of one of even numbered SEQ ID NOs: 2-112;
- (b) a nucleic acid molecule comprising a nucleic acid sequence of one of odd numbered SEQ ID NOs: 1-111;
- 10 (c) a nucleic acid molecule that has a nucleic acid sequence at least 90% identical to the nucleic acid sequence of the nucleic acid molecule of (a) or (b) ;
- (d) a nucleic acid molecule that hybridizes to (a) or (b) under conditions of hybridization selected from the group consisting of:
 - 15 (i) 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM ethylenediamine tetraacetic acid (EDTA) at 50°C with a final wash in 2X standard saline citrate (SSC), 0.1% SDS at 50°C;
 - (ii) 7% SDS, 0.5 M NaPO₄, 1 mM EDTA at 50°C with a final wash in 1X SSC, 0.1% SDS at 50°C;
 - 20 (iii) 7% SDS, 0.5 M NaPO₄, 1 mM EDTA at 50°C with a final wash in 0.5X SSC, 0.1% SDS at 50°C;
 - (iv) 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with a final wash in 0.1X SSC, 0.1% SDS at 50°C; and
 - 25 (v) 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with a final wash in 0.1X SSC, 0.1% SDS at 65°C;
- 30 (e) a nucleic acid molecule comprising a nucleic acid sequence fully complementary to (a); and

- (f) a nucleic acid molecule comprising a nucleic acid sequence that is the full reverse complement of (a).

17. An isolated stress-related polypeptide encoded by the isolated nucleic acid molecule of claim 16, or a functional fragment, domain, or
5 feature thereof.

18. A method for producing a polypeptide of claim 17, comprising the steps of:

- (a) growing cells comprising an expression cassette under suitable growth conditions, the expression cassette comprising a
10 nucleic acid molecule of claim 16; and
(b) isolating the polypeptide from the cells.

19. A transgenic plant cell comprising an isolated nucleic acid molecule of claim 1.

20. The transgenic plant of claim 19, wherein the plant is selected
15 from the group consisting of corn (*Zea mays*), *Brassica* sp., alfalfa (*Medicago sativa*), rice (*Oryza sativa* ssp.), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanut (*Arachis hypogaea*), cotton, sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Coffea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea
20 (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea ultilane*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats,
25 duckweed (*Lemna*), barley, a vegetable, an ornamental, and a conifer.

21. The transgenic plant of claim 20, wherein the plant is rice (*Oryza sativa* ssp.)

22. The transgenic plant of claim 20, wherein the duckweed is selected from the group consisting of genus *Lemna*, genus *Spirodela*, genus
5 *Woffia*, and genus *Wofsiella*.

23. The transgenic plant of claim 20, wherein the vegetable is selected from the group consisting of tomatoes, lettuce, guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, green bean, lima bean, pea, and members of the genus *Cucumis*.

10 24. The transgenic plant of claim 20, wherein the ornamental is selected from the group consisting of impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum,
15 Mesembryanthemum, Salpiglossos, and Zinnia, azalea, hydrangea, hibiscus, rose, tulip, daffodil, petunia, carnation, poinsettia, and chrysanthemum.

25. The transgenic plant of claim 20, wherein the conifer is selected from the group consisting of loblolly pine, slash pine, ponderosa pine, lodgepole pine, Monterey pine, Douglas-fir, Western hemlock, Sitka spruce,
20 redwood, silver fir, balsam fir, Western red cedar, and Alaska yellow-cedar.

26. The transgenic plant of claim 19, wherein the transgenic plant is a plant selected from the group consisting of Acacia, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra,
25 orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, *Brassica*, broccoli, cabbage, ultilan sprouts,
30 onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, ultilane, and zucchini.

27. An isolated stress-related polypeptide, wherein the polypeptide binds in a yeast two hybrid assay to a fragment of a protein selected from the group consisting of OsGF14-c (SEQ ID NO: 113), OsDAD1 (SEQ ID NO: 128), Os006819-2510 (SEQ ID NO: 20), OsCRTC (SEQ ID NO: 134),
5 OsSGT1 (SEQ ID NO: 144), OsERP (SEQ ID NO: 146), OsCHIB1 (SEQ ID NO: 152), OsCS (SEQ ID NO: 156), OsPP2A-2 (SEQ ID NO: 164), and OsCAA90866 (SEQ ID NO: 170).

28. The isolated stress-related polypeptide of claim 17, wherein the isolated stress-related polypeptide is selected from the group consisting of:

- 10 (a) a polypeptide comprising an amino acid sequence of even numbered SEQ ID NOs: 2-112; and
(b) a polypeptide comprising an amino acid sequence at least 80% similar to the polypeptide of (a) using the GCG Wisconsin Package SEQWEB® application of GAP with the default GAP
15 analysis parameters.

29. The isolated stress-related polypeptide of claim 28, wherein the polypeptide comprises an amino acid sequence of one of even numbered SEQ ID NOs: 2-112.

30. An expression cassette comprising a nucleic acid molecule
20 encoding a stress-related polypeptide of claim 1.

31. The expression cassette of claim 30, wherein the nucleic acid molecule encoding a stress-related polypeptide comprises a nucleic acid sequence selected from odd numbered SEQ ID NOs: 1-111.

32. The expression cassette of claim 30, wherein the expression
25 cassette further comprises a regulatory element operatively linked to the nucleic acid molecule.

33. The expression cassette of claim 32, wherein the regulatory element comprises a promoter.

34. The expression cassette of claim 33, wherein the promoter is a
30 plant promoter.

35. The expression cassette of claim 33, wherein the promoter is a constitutive promoter.

36. The expression cassette of claim 33, wherein the promoter is a tissue-specific or a cell type-specific promoter.

5 37. The expression cassette of claim 36, wherein the tissue-specific or cell type-specific promoter directs expression of the expression cassette in a location selected from the group consisting of epidermis, root, vascular tissue, meristem, cambium, cortex, pith, leaf, flower, seed, and combinations thereof.

10 38. A transgenic plant cell comprising the expression cassette of claim 30.

39. The transgenic plant cell of claim 38, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence of one of odd numbered SEQ ID NOs: 1-111.

15 40. A transgenic plant comprising the expression cassette of claim 30.

41. Transgenic seeds or progeny of the transgenic plant of claim 40.

42. A method for modulating stress response of a plant cell comprising introducing into the plant cell an expression cassette comprising an isolated nucleic acid molecule encoding a stress-related polypeptide, wherein the
20 polypeptide binds in a yeast two hybrid assay to a fragment of a protein selected from the group consisting of OsGF14-c (SEQ ID NO: 113), OsDAD1 (SEQ ID NO: 128), Os006819-2510 (SEQ ID NO: 20), OsCRTC (SEQ ID NO : 134), OsSGT1 (SEQ ID NO: 144), OsERP (SEQ ID NO: 146), OsCHIB1 (SEQ ID NO: 152), OsCS (SEQ ID NO: 156), OsPP2A-2 (SEQ ID
25 NO: 164), and OsCAA90866 (SEQ ID NO: 170).

43. The method of claim 42, wherein expression of the polypeptide in the cell results in an enhancement of a rate or extent of proliferation of the cell.

44. The method of claim 42, wherein expression of the polypeptide in
30 the cell results in a decrease in a rate or extent of proliferation of the cell.

45. The method of claim 42, wherein the isolated nucleic acid molecule comprises a nucleic acid sequence selected from one of odd numbered SEQ ID NOs: 1-173.

46. The method of claim 45, wherein the isolated nucleic acid
5 molecule comprises a nucleic acid sequence selected from one of odd numbered SEQ ID NOs: 1-111.